

AMENDMENTS

Amendments to the Specification

Please delete paragraph [0102] of the specification, found on pages 34-35, and replace it with the following:

[0102] For the purposes of the invention, the percent sequence identity between two nucleic acid or polypeptide sequences may be determined using the "Blast Two Sequences" program available from the at National Center for Biotechnology Information, division of the National Library of Medicine (NLM) at the National Institutes of Health (NIH) (<http://www.ncbi.nlm.nih.gov/blast/bl2seq/bl2.html>). The percent sequence identity of two nucleic acids is determined using the algorithm of Karlin & Altschul, 1990 Proc. Natl. Acad. Sci. USA 87:2264-2268, modified as in Karlin & Altschul, 1993 Proc. Natl. Acad. Sci. USA 90:5873-5877. Such an algorithm is incorporated into the NBLAST and XBLAST programs of Altschul *et al.*, 1990 J. Mol. Biol. 215:402-410. BLAST nucleotide searches are performed with the NBLAST program, score = 100, wordlength = 12, to obtain nucleotide sequences with the desired percent sequence identity. To obtain gapped alignments for comparison purposes, Gapped BLAST is used as described in Altschul *et al.*, 1997 Nucl. Acids. Res. 25:3389-3402. When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs (NBLAST and XBLAST) are used. See <http://www.ncbi.nih.gov/>. It is to be understood that for the purposes of determining sequence identity when comparing a DNA sequence to an RNA sequence, a thymidine nucleotide is equivalent to a uracil nucleotide.